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<p>(21) International Application Number: PCT/US98/04376 (22) International Filing Date: 27 February 1998 (27.02.98) (30) Priority Data: 08/812,994 4 March 1997 (04.03.97) US (71) Applicant: VENTANA GENETICS, INC. [US/US]; Suite 201, 421 Wakara Way, Salt Lake City, UT 84108 (US). (72) Inventors: KAMB, Carl, Alexander; 1103 East 600 South, Salt Lake City, UT 84102 (US). PORITZ, Mark, A.; 584 - 18th Avenue, Salt Lake City, UT 84103 (US). (74) Agents: SHUSTER, Michael, J. et al.; McCutchen, Doyle, Brown & Enersen, Three Embarcadero Center, San Francisco, CA 94111 (US).</p>		<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>
<p>(54) Title: METHODS FOR IDENTIFYING NUCLEIC ACID SEQUENCES ENCODING AGENTS THAT AFFECT CELLULAR PHENOTYPES</p> <p>(57) Abstract</p> <p>Methods for identifying nucleic acid sequences that affect a cellular phenotype are disclosed. The method uses a reporter gene whose level of expression correlates with the phenotype in conjunction with a method or device for measuring the level of reporter expression. An expression library is introduced into the cells, and those cells exhibiting changes in reporter expression level are selected. Expression library inserts from the selected cells are isolated, thereby providing a sub-library enriched for sequences that affect the phenotype reflected by the reporter. Further rounds of sub-library introduction and cell selection may be carried out to provide additional enrichment. Sequences identified using this method may be used to ascertain the identity of additional molecules involved in generating the cellular phenotype.</p>		